OS-90
0417

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/076,157

DATE: 04/16/2002
TIME: 14:33:26

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04162002\J076157.raw**

```
 3 <110> APPLICANT: Pompejus, Markus
 4         Suelberger, Harald
 5         Joeffken, Hans Wolfgang
 6         Doval, Jose Luis Revuelta
 7         Jimenez, Alberto;
 8         Garcia, Maria Angeles Santos
10 <120> TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii and the
use thereof
11         in
12         microbial riboflavin synthesis
14 <130> FILE REFERENCE: 48684DIV
16 <140> CURRENT APPLICATION NUMBER: US 10/076,157
17 <141> CURRENT FILING DATE: 2002-02-15
19 <150> PRIOR APPLICATION NUMBER: US 09/212,247
20 <151> PRIOR FILING DATE: 1998-12-16
22 <160> NUMBER OF SEQ ID NOS: 21
24 <170> SOFTWARE: WordPerfect v. 6.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1911
28 <212> TYPE: DNA
29 <213> ORGANISM: Ashbya gosypii
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: 626..1582
35 <400> SEQUENCE: 1
37 ggtagtcgct catcgacaga cacaatcgcg tgttctctct gaatcgtcca ttgggtgtca      60
39 gcatcctgat cgcgggcgga tggaatgggt aatcattagg aaacaccaat gtcccatggt     120
41 attgtccgtc ctcgtatggt gtctcaggag gacccgtgat cacgtagtgc cacaccagga     180
43 tattgtcttc ctttggtgct gccacgatgt agggcggggg gttctcggtc atcattttgt     240
45 actcctttga gagccgcttg tacgcctgtc ttgatgccat cttgcctact attagtttct     300
47 caccacttcc cgccaaacaa tctgcacttt acgagcgcta tctatccctc gggtcgctct     360
49 agttgattat tggcgaaact gatagttcag gtacttccat gatgcggtca tatccacgta     420
51 tgtgatcacg tgatcatcag ccatgctgcc agctcacggg cctgcctaca ctattggagg     480
53 ctctgtgagt catgatttat tgcatatcaa gcccagatag tcgttgggga tactaccgtt     540
55 gccgcgatga gctccgatat taagttgtag ccaaaaattt taacggatga cttcttaaca     600
57 gttattgacg ccgcaatcct acgcc atg tcg tcc aat agc ata aag ctg cta     652
58                                Met Ser Ser Asn Ser Ile Lys Leu Leu
59                                 1               5
61 gca ggt aac tcg cac ccg gac cta gct gag aag gtc tcc gtt cgc cta     700
62 Ala Gly Asn Ser His Pro Asp Leu Ala Glu Lys Val Ser Val Arg Leu
63  10              15                  20                  25
65 ggt gta cca ctt tcg aag att gga gtg tat cac tac tct aac aaa gag     748
66 Gly Val Pro Leu Ser Lys Ile Gly Val Tyr His Tyr Ser Asn Lys Glu
67              30                  35                  40
```

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69 acg tca gtt act atc ggc gaa agt atc cgt gat gaa gat gtc tac atc        796
70 Thr Ser Val Thr Ile Gly Glu Ser Ile Arg Asp Glu Asp Val Tyr Ile
71            45                  50                  55
73 atc cag aca gga acg ggg gag cag gaa atc aac gac ttc ctc atg gaa        844
74 Ile Gln Thr Gly Thr Gly Glu Gln Glu Ile Asn Asp Phe Leu Met Glu
75            60                  65                  70
77 ctg ctc atc atg atc cat gcc tgc cgg tca gcc tct gcg cgg aag atc        892
78 Leu Leu Ile Met Ile His Ala Cys Arg Ser Ala Ser Ala Arg Lys Ile
79     75                  80                  85
81 aca gcg gtt ata cca aac ttc cct tac gca aga caa gac aaa aag gac        940
82 Thr Ala Val Ile Pro Asn Phe Pro Tyr Ala Arg Gln Asp Lys Lys Asp
83 90                  95                 100                 105
85 aag tcg cga gca ccg ata act gcc aag ctg gtg gcc aag atg cta gag        988
86 Lys Ser Arg Ala Pro Ile Thr Ala Lys Leu Val Ala Lys Met Leu Glu
87                110                 115                 120
89 acc gcg ggg tgc aac cac gtt atc acg atg gat ttg cac gcg tct caa       1036
90 Thr Ala Gly Cys Asn His Val Ile Thr Met Asp Leu His Ala Ser Gln
91                125                 130                 135
93 att cag ggt ttc ttc cac att cca gtg gac aac cta tat gca gag ccg       1084
94 Ile Gln Gly Phe Phe His Ile Pro Val Asp Asn Leu Tyr Ala Glu Pro
95            140                 145                 150
97 aac atc ctg cac tac atc caa cat aat gtg gac ttc cag aat agt atg       1132
98 Asn Ile Leu His Tyr Ile Gln His Asn Val Asp Phe Gln Asn Ser Met
99     155                 160                 165
101 ttg gtc gcg cca gac gcg ggg tcg gcg aag cgc acg tcg acg ctt tcg      1180
102 Leu Val Ala Pro Asp Ala Gly Ser Ala Lys Arg Thr Ser Thr Leu Ser
103 170                 175                 180                 185
105 gac aag ctg aat ctc aac ttc gcg ttg atc cac aaa gaa cgg cag aag      1228
106 Asp Lys Leu Asn Leu Asn Phe Ala Leu Ile His Lys Glu Arg Gln Lys
107                190                 195                 200
109 gcg aac gag gtc tcg cgg atg gtg ttg gtg ggt gat gtc gcc gac aag      1276
110 Ala Asn Glu Val Ser Arg Met Val Leu Val Gly Asp Val Ala Asp Lys
111                205                 210                 215
113 tcc tgt att att gta gac gac atg gcg gac acg tgc gga acg cta gtg      1324
114 Ser Cys Ile Ile Val Asp Asp Met Ala Asp Thr Cys Gly Thr Leu Val
115            220                 225                 230
117 aag gcc act gac acg ctg atc gaa aat tgt gcg aaa gaa gtg att gcc      1372
118 Lys Ala Thr Asp Thr Leu Ile Glu Asn Cys Ala Lys Glu Val Ile Ala
119     235                 240                 245
121 att gtg aca cac ggt ata ttt tct ggc ggc gcc cgc gag aag ttg cgc      1420
122 Ile Val Thr His Gly Ile Phe Ser Gly Gly Ala Arg Glu Lys Leu Arg
123 250                 255                 260                 265
125 aac agc aag ctg gca cgg atc gta agc aca aat acg gtg cca gtg gac      1468
126 Asn Ser Lys Leu Ala Arg Ile Val Ser Thr Asn Thr Val Pro Val Asp
127                270                 275                 280
129 ctc aat cta gat atc tac cac caa att gac att agt gcc att ttg gcc      1516
130 Leu Asn Leu Asp Ile Tyr His Gln Ile Asp Ile Ser Ala Ile Leu Ala
131            285                 290                 295
133 gag gca att aga agg ctt cac aac ggg gaa agt gtg tcg tac ctg ttc      1564
```

```
134 Glu Ala Ile Arg Arg Leu His Asn Gly Glu Ser Val Ser Tyr Leu Phe
135         300             305             310
137 aat aac gct gtc atg tagtgctgtc agtggcagat gcatgatcgc tggcctaatt        1619
138 Asn Asn Ala Val Met
139     315
141 atctgtgtaa gttgatacaa tgcagtaaat acagtacata aaactgaatg tttttcactt        1679
143 aggggtgctt tgttgttctg atagcgtgtg tgcgaatttg gaggtgaaag ttgaacatca        1739
145 cgtaatgaat acaaacaaga ttgcacatta ggaaaagcga taaattattt attatttgca        1799
147 actggccttt gagcgtttaa gcctgaacat ttttgccctt ttgtttgacc gtaccgttat        1859
149 cactcgtcct tatatatggc tatccttctc ttccggaact tcttcgagcg ta               1911
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 318
156 <212> TYPE: PRT
157 <213> ORGANISM: Ashbya gosypii
159 <400> SEQUENCE: 2
161 Met Ser Ser Asn Ser Ile Lys Leu Leu Ala Gly Asn Ser His Pro Asp
162 1               5               10              15
164 Leu Ala Glu Lys Val Ser Val Arg Leu Gly Val Pro Leu Ser Lys Ile
165         20              25              30
167 Gly Val Tyr His Tyr Ser Asn Lys Glu Thr Ser Val Thr Ile Gly Glu
168         35              40              45
170 Ser Ile Arg Asp Glu Asp Val Tyr Ile Ile Gln Thr Gly Thr Gly Glu
171     50              55              60
173 Gln Glu Ile Asn Asp Phe Leu Met Glu Leu Leu Ile Met Ile His Ala
174 65              70              75              80
176 Cys Arg Ser Ala Ser Ala Arg Lys Ile Thr Ala Val Ile Pro Asn Phe
177             85              90              95
179 Pro Tyr Ala Arg Gln Asp Lys Lys Asp Lys Ser Arg Ala Pro Ile Thr
180         100             105             110
182 Ala Lys Leu Val Ala Lys Met Leu Glu Thr Ala Gly Cys Asn His Val
183         115             120             125
185 Ile Thr Met Asp Leu His Ala Ser Gln Ile Gln Gly Phe Phe His Ile
186     130             135             140
188 Pro Val Asp Asn Leu Tyr Ala Glu Pro Asn Ile Leu His Tyr Ile Gln
189 145             150             155             160
191 His Asn Val Asp Phe Gln Asn Ser Met Leu Val Ala Pro Asp Ala Gly
192             165             170             175
194 Ser Ala Lys Arg Thr Ser Thr Leu Ser Asp Lys Leu Asn Leu Asn Phe
195             180             185             190
197 Ala Leu Ile His Lys Glu Arg Gln Lys Ala Asn Glu Val Ser Arg Met
198         195             200             205
200 Val Leu Val Gly Asp Val Ala Asp Lys Ser Cys Ile Ile Val Asp Asp
201     210             215             220
203 Met Ala Asp Thr Cys Gly Thr Leu Val Lys Ala Thr Asp Thr Leu Ile
204 225             230             235             240
206 Glu Asn Cys Ala Lys Glu Val Ile Ala Ile Val Thr His Gly Ile Phe
207             245             250             255
209 Ser Gly Gly Ala Arg Glu Lys Leu Arg Asn Ser Lys Leu Ala Arg Ile
210             260             265             270
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```
212 Val Ser Thr Asn Thr Val Pro Val Asp Leu Asn Leu Asp Ile Tyr His
213          275             280             285
215 Gln Ile Asp Ile Ser Ala Ile Leu Ala Glu Ala Ile Arg Arg Leu His
216          290                 295             300
218 Asn Gly Glu Ser Val Ser Tyr Leu Phe Asn Asn Ala Val Met
219 305                 310             315
223 <210> SEQ ID NO: 3
224 <211> LENGTH: 5369
225 <212> TYPE: DNA
226 <213> ORGANISM: Ashbya gossypii
228 <220> FEATURE:
229 <221> NAME/KEY: CDS
230 <222> LOCATION: 55..1482
232 <220> FEATURE:
233 <221> NAME/KEY: CDS
234 <222> LOCATION: 1767..3299
236 <220> FEATURE:
237 <221> NAME/KEY: CDS
238 <222> LOCATION: 3588..4703
240 <400> SEQUENCE: 3
242 aagcttgacc ttggctggca cttgagtcgg cagacaggtg gactaacccg agca atg      57
243                                                               Met
244                                                                 1
246 gat cgt ggt tgt aaa ggt atc tct tat gtg ctc agt gca atg gtt ttt     105
247 Asp Arg Gly Cys Lys Gly Ile Ser Tyr Val Leu Ser Ala Met Val Phe
248              5                  10              15
250 cac ata ata ccg att aca ttt gaa ata tcg atg gta tgt ggc ata ttg     153
251 His Ile Ile Pro Ile Thr Phe Glu Ile Ser Met Val Cys Gly Ile Leu
252          20                  25              30
254 aca tac cag ttt ggt gct tcc ttc gct gct ata aca ttc tcg act atg     201
255 Thr Tyr Gln Phe Gly Ala Ser Phe Ala Ala Ile Thr Phe Ser Thr Met
256      35              40              45
258 ctt ctt tac tcc atc ttt act ttc aga acg acg gcg tgg cgc aca cgg     249
259 Leu Leu Tyr Ser Ile Phe Thr Phe Arg Thr Thr Ala Trp Arg Thr Arg
260  50              55              60                  65
262 ttt agg cgt gat gcg aac aag gct gac aat aag gcc gct agt gtg gca     297
263 Phe Arg Arg Asp Ala Asn Lys Ala Asp Asn Lys Ala Ala Ser Val Ala
264              70                  75              80
266 ttg gat tcc cta ata aat ttt gaa gct gta aag tat ttc aat aac gag     345
267 Leu Asp Ser Leu Ile Asn Phe Glu Ala Val Lys Tyr Phe Asn Asn Glu
268              85                  90              95
270 aag tac ctt gcg gac aag tat cac aca tcc ttg atg aag tac cgg gat     393
271 Lys Tyr Leu Ala Asp Lys Tyr His Thr Ser Leu Met Lys Tyr Arg Asp
272          100             105             110
274 tcc cag ata aag gtc tcg caa tcg ctg gcg ttt ttg aac acc ggc cag     441
275 Ser Gln Ile Lys Val Ser Gln Ser Leu Ala Phe Leu Asn Thr Gly Gln
276          115             120             125
278 aac cta att ttt acc act gca ctg act gca atg atg tat atg gcc tgt     489
279 Asn Leu Ile Phe Thr Thr Ala Leu Thr Ala Met Met Tyr Met Ala Cys
```

```
280 130                        135                    140                      145
282 aat ggt gtt atg cag ggc tct ctt aca gtg ggg gat ctt gtg tta att          537
283 Asn Gly Val Met Gln Gly Ser Leu Thr Val Gly Asp Leu Val Leu Ile
284                             150                    155                 160
286 aat caa ctg gta ttc cag ctc tcc gtg cca cta aac ttc ctt ggt agc          585
287 Asn Gln Leu Val Phe Gln Leu Ser Val Pro Leu Asn Phe Leu Gly Ser
288                        165                    170                  175
290 gtc tac cgt gat ctc aag cag tct ctg ata gat atg gaa tct tta ttt          633
291 Val Tyr Arg Asp Leu Lys Gln Ser Leu Ile Asp Met Glu Ser Leu Phe
292             180                        185                 190
294 aaa ctg caa aaa aat cag gtc aca att aag aac tcc cca aat gcc cag          681
295 Lys Leu Gln Lys Asn Gln Val Thr Ile Lys Asn Ser Pro Asn Ala Gln
296        195                        200                    205
298 aac cta cca ata cac aaa ccg ttg gat att cgc ttt gaa aat gtt acg          729
299 Asn Leu Pro Ile His Lys Pro Leu Asp Ile Arg Phe Glu Asn Val Thr
300 210                         215                    220                  225
302 ttt ggc tat gac ccg gag cgg cgt ata ttg aac aat gtt tcg ttt acc          777
303 Phe Gly Tyr Asp Pro Glu Arg Arg Ile Leu Asn Asn Val Ser Phe Thr
304                             230                    235                  240
306 atc cca gct gga atg aag act gcc ata gta ggc cca tcg ggc tcg ggg          825
307 Ile Pro Ala Gly Met Lys Thr Ala Ile Val Gly Pro Ser Gly Ser Gly
308                        245                    250                  255
310 aag tcc acc att ttg aag ctc gta ttt aga ttc tat gag ccc gag caa          873
311 Lys Ser Thr Ile Leu Lys Leu Val Phe Arg Phe Tyr Glu Pro Glu Gln
312             260                    265                    270
314 ggt cgt atc cta gtt ggc ggc aca gat atc cgc gat tta gac ttg ctt          921
315 Gly Arg Ile Leu Val Gly Gly Thr Asp Ile Arg Asp Leu Asp Leu Leu
316        275                        280                    285
318 tct tta cgg aag gct atc ggt gtc gtg ccc caa gat act cct ctc ttc          969
319 Ser Leu Arg Lys Ala Ile Gly Val Val Pro Gln Asp Thr Pro Leu Phe
320 290                         295                    300                  305
322 aat gac aca atc tgg gag aat gtt aaa ttc ggc aat atc agt tcc tct          1017
323 Asn Asp Thr Ile Trp Glu Asn Val Lys Phe Gly Asn Ile Ser Ser Ser
324                             310                    315                  320
326 gac gat gag att ctc agg gcc ata gaa aaa gct caa ctc acg aag cta          1065
327 Asp Asp Glu Ile Leu Arg Ala Ile Glu Lys Ala Gln Leu Thr Lys Leu
328                        325                    330                  335
330 ctc cag aac cta cca aag ggc gct tcc acc gtt gta ggg gag cgc ggt          1113
331 Leu Gln Asn Leu Pro Lys Gly Ala Ser Thr Val Val Gly Glu Arg Gly
332             340                    345                    350
334 ttg atg atc agc gga ggt gag aaa caa agg ctt gct att gct cgt gtg          1161
335 Leu Met Ile Ser Gly Gly Glu Lys Gln Arg Leu Ala Ile Ala Arg Val
336        355                    360                    365
338 ctt ttg aag gac gct ccg ctg atg ttt ttc gac gag gct aca agt gct          1209
339 Leu Leu Lys Asp Ala Pro Leu Met Phe Phe Asp Glu Ala Thr Ser Ala
340 370                        375                    380                  385
342 ctg gat aca cac aca gag cag gca ctc ttg cac acc att cag cag aac          1257
343 Leu Asp Thr His Thr Glu Gln Ala Leu Leu His Thr Ile Gln Gln Asn
344                        390                    395                  400
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/076,157

DATE: 04/16/2002
TIME: 14:33:28

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04162002\J076157.raw**